Amendment to the Specification:

Please amend the specification as indicated.

Please replace the paragraph at page 9, line 34 to page 10, line 14 with the following paragraph:

--Percent (%) amino acid sequence identity" with respect to the CHEPO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in a CHEPO sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are obtained as described below by using the sequence comparison computer program ALIGN-2~~, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below~~. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code ~~shown in Table 1~~ has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, Calif.~~ or may be compiled from the source code provided in Table 1~~. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.--

Please replace the paragraph at page 10, lines 15-26 with the following paragraph:

--For purposes herein, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations, Tables 1 and 2 ~~2 and 3~~ below demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO".--

Please replace the paragraph at page 12, lines 8-24 with the following paragraph:

--Percent (%) nucleic acid sequence identity" with respect to the CHEPO polypeptide-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in a CHEPO polypeptide-encoding nucleic acid sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN, ALIGN-2 or Megalign (DNASTAR) software. Those skilled in the art can determine

appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full-length of the sequences being compared. For purposes herein, however, % nucleic acid sequence identity values are obtained as described below by using the sequence comparison computer program ALIGN-2, ~~wherein the complete source code for the ALIGN-2 program is provided in Table 1~~. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code ~~shown in Table 1~~ has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, Calif. ~~or may be compiled from the source code provided in Table 1~~. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.--

Please replace the paragraph at page 12, line 25 to page 13, line 2 with the following paragraph:

--For purposes herein, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables <u>3 and 4</u> 4 ~~and 5~~ below demonstrate how to calculate the % nucleic acid sequence identity of the

nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA".--

At page 19 - 40, delete Table 1.

Please replace the following tables at pages 41 and 42 with the following:

--Table 1 ~~Table 2~~

PRO	XXXXXXXXXXXXXXX	(Length = 15 amino acids)
Comparison Protein	XXXXXYYYYYYY	(Length = 12 amino acids)

% amino acid sequence identity =
(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =
5 divided by 15 = 33.3%

Table 2 ~~Table 3~~

PRO	XXXXXXXXXX	(Length = 10 amino acids)
Comparison Protein	XXXXXYYYYYYZZYZ	(Length = 15 amino acids)

% amino acid sequence identity =
(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =
5 divided by 10 = 50%

Table 3 ~~Table 4~~

PRO-DNA	NNNNNNNNNNNNN	(Length = 14 nucleotides)
Comparison DNA	NNNNNNLLLLLLLLL	(Length = 16 nucleotides)

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =
6 divided by 14 = 42.9%

Table 4 ~~**Table 5**~~

PRO-DNA	NNNNNNNNNNNN	(Length = 12 nucleotides)
Comparison DNA	NNNNLLLVV	(Length = 9 nucleotides)

% nucleic acid sequence identity =
(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =
4 divided by 12 = 33.3%--

Please replace the following paragraph and table at page 44, lines 4-33 with the following:

--In particular embodiments, conservative substitutions of interest are shown in Table 5 ~~6~~ under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 5 ~~6~~, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 5 ~~Table 6~~

Original Residue	Exemplary Substitutions	Preferred Substitutions
Ala (A)	val; leu; ile	val
Arg (R)	lys; gln; asn	lys
Asn (N)	gln; his; lys; arg	gln
Asp (D)	glu	glu
Cys (C)	ser	ser
Gln (Q)	asn	asn
Glu (E)	asp	asp
Gly (G)	pro; ala	ala
His (H)	asn; gln; lys; arg	arg
Ile (I)	leu; val; met; ala; phe; norleucine	leu
Leu (L)	norleucine; ile; val; met; ala; phe	ile
Lys (K)	arg; gln; asn	arg
Met (M)	leu; phe; ile	leu
Phe (F)	leu; val; ile; ala; tyr	leu
Pro (P)	ala	ala
Ser (S)	thr	thr
Thr (T)	ser	ser
Trp (W)	tyr; phe	tyr
Tyr (Y)	trp; phe; thr; ser	phe
Val (V)	ile; leu; met; phe; ala; norleucine	leu--

Please replace the paragraph at page 49, lines 10-11 with the following paragraph:

--Variations in the native sequence as described above can be made using any of the techniques and guidelines for conservative and non-conservative mutations set forth in Table 5 ~~6~~ above.--

Please replace the paragraphs and tables at page 87, line 17 to page 88, line 25 with the following paragraphs and tables:

--In an alternate assay for measuring the biological activity of the CHEPO-IgG1 immunoadhesin, stimulation of the production of erythroid colonies by CHEPO-IgG1

was monitored in human bone marrow cells. Fresh human bone marrow aspirates were obtained from healthy donors (Poietic Technologies, Gaithersburg, Md.). The mononuclear fraction was enriched for CD34 by immunomagnetic positive selection. Methylcellulose cultures were initiated with 1000 cells in complete methylcellulose media without erythropoietin (Stem Cell Technologies, Vancuver, BC). Culture medium was later supplemented with 50 ng/mL rhEpo or CHEPO-IgG1 and 50 ng/ml of kit ligand (KL), which acts as a stem cell factor (also called scf), and synergizes in these assays with Epo to promote the formation of arythroid colonies. After 12-14 days, colonies were enumerated and phenotyped on an inverted light microscope. The efficiency of CHEPO-IgG1 in stimulating production of erythroid colonies from human bone marrow cells was measured and compared to the results from assays with rhEPO. Colony numbers from quadruplicate plates and repeated in two independent experiments are presented in the following Table 6 ~~7~~.

TABLE 6

Experiment #1	BFU-E	CFU-GEMM	CFU-GM	Macrophage
KL/rhEpo	88	0	0	0
KL/CHEPO-IgG1	82	0	1	0

Experiment #2	BFU-E	CFU-GEMM	CFU-GM	Macrophage
KL/rhEpo	104	0	0	0
KL/CHEPO-IgG1	92	0	0	0

BFU-E: burst-forming unit erythroid

CFU-GEMM: colony-forming unit-granulocyte, erythroid, macrophage, megakaryocyte

CFU-GM: colony-forming unit-glanulocyte-macrophage

KL: kit ligand

C. Stimulation of bone marrow cells in liquid culture

The biological activity of CHEPO-IgG1was assessed in a third assay, measuring stimulation of bone marrow cells in liquid culture. Twenty thousand CD34+ cells isolated as described above were cultured in IMDM/10% FCS in the presence of CF, 50 ng/ml of kit ligand (KL) and either 50 ng/mL rhEpo (Amgen) or CHEPO-IgG1. 7-10 inch plates of culture cells were counted by a hematocytometer and subsequently assayed for expression of the erythroid cell surface markers CD36, CD71 and Glycophorin A. As shown in Table 7 ~~8~~ and FIG. 5, CHEPO-IgG1 was as efficient as rhEPO in stimulating the formation of immature and mature erythroid cells in bone marrow liquid culture.

TABLE 7

Condition	Total cellularity
KL	2.50+05
KL/rhEPO	2.20E+06
KL/CHEPO-IgG1	2.06+06

KL: kit ligand--